

0257

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/029,905

DATE: 01/15/2002

TIME: 08:04:57

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3 <110> APPLICANT: Boehringer Ingelheim Pharma KG
 5 <120> TITLE OF INVENTION: Method for identifying compounds which positively
 6 influence inflammatory conditions
 8 <130> FILE REFERENCE: 1/1177
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/029,905
 C--> 11 <141> CURRENT FILING DATE: 2001-12-21
 13 <150> PRIOR APPLICATION NUMBER: US 60/257,854
 14 <151> PRIOR FILING DATE: 2000-12-22
 16 <160> NUMBER OF SEQ ID NOS: 12
 18 <170> SOFTWARE: PatentIn Ver. 2.1
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 22 <212> TYPE: DNA
 23 <213> ORGANISM: Artificial Sequence
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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 36 <213> ORGANISM: Artificial Sequence
 38 <220> FEATURE:
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 46 <211> LENGTH: 1819
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Homo sapiens
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 52 aaaatcatct ccatattctc aggcacagag aaaggaagta aaaagaaaga aaaggaacgg 120
 53 ccagaaatct ctctccatc tgattttgag cacaccatcc atgttggtt tgatactgtt 180
 54 actggagaat tcaactggcat gccagaacag tgggtctgat tactacagac ctccaatata 240
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 60 gatggtgctg ccaagtcttt agacaaacag aaaaagaaga ctaagatgac agatgaagag 600
 61 attatggaga aattaagaac tatcgtgagc ataggtgacc ctaagaaaaa atatacaaga 660
 62 tatgaaaaaa ttggacaagg ggcttctggt acagttttca ctgctactga cgttgactgt 720
 63 ggacaggagg ttgctatcaa acaaattaat ttacagaaac agccaaagaa ggaactgatc 780
 64 attaacgaga ttctggtgat gaaagaattg aaaaatccca acatcgtaa ctttttggac 840
 65 agttacctgg taggagatga attgtttgtg gtcattggaat acctgtctgg gaggtcactc 900

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68 gacaatgtac ttttgggaat ggaaggatct gttaagctca ctgactttgg tttctgtgcc 1080
69 cagatcacc ctagcagag caaacgcagt accatggctg gaacgccata ctggatggca 1140
70 ccagaggtgg ttacacggaa agcttatggc cctaaagtcg acatatggtc tctgggtatc 1200
71 atggctattg agatggtaga aggagagcct ccatacctca atgaaaatcc ccttagggcc 1260
72 ttgtacctaa tagcaactaa tggaacccca gaacttcaga atccagagaa actttcccca 1320
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74 aaagaattat tacagcatcc tttcctgaaa ctggccaaac cgttatctag ctgacacca 1440
75 ctgatcatgg cagctaaaga agcaatgaag agtaaccgtt aacatcactg ctgtggcctc 1500
76 atactctttt ttccattttc tacaagaagc cttttagtat atgaaaatta ttactctttt 1560
77 tggggtttta agaaatggtc tgcataacct gaatgaaaga agcaaatgac tattctctga 1620
78 agacaaccaa gagaaaattg caaaaagaca agtatgactt ttatatgaac cccttcttta 1680
79 ggggtccagaa ggaattgtgg actgaatcac tagccttagg tctttcagca aacagcctat 1740
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81 cccattcatt gtccccctt                                     1819
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87 <213> ORGANISM: Homo sapiens
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94           20           25           30
96 Ala Asn His Ser Leu Lys Pro Leu Pro Ser Val Pro Glu Glu Lys Lys
97           35           40           45
99 Pro Arg His Lys Ile Ile Ser Ile Phe Ser Gly Thr Glu Lys Gly Ser
100          50           55           60
102 Lys Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Pro Pro Ser Asp Phe
103          65           70           75           80
105 Glu His Thr Ile His Val Gly Phe Asp Ala Val Thr Gly Glu Phe Thr
106           85           90           95
108 Gly Met Pro Glu Gln Trp Ala Arg Leu Leu Gln Thr Ser Asn Ile Thr
109           100          105          110
111 Lys Leu Glu Gln Lys Lys Asn Pro Gln Ala Val Leu Asp Val Leu Lys
112           115          120          125
114 Phe Tyr Asp Ser Asn Thr Val Lys Gln Lys Tyr Leu Ser Phe Thr Pro
115           130          135          140
117 Pro Glu Lys Asp Gly Leu Pro Ser Gly Thr Pro Ala Leu Asn Ala Lys
118          145          150          155          160
120 Gly Thr Glu Ala Pro Ala Val Val Thr Glu Glu Asp Asp Asp Glu
121           165          170          175
123 Glu Thr Ala Pro Pro Val Ile Ala Pro Arg Pro Asp His Thr Lys Ser
124           180          185          190
126 Ile Tyr Thr Arg Ser Val Ile Asp Pro Val Pro Ala Pro Val Gly Asp
127           195          200          205
129 Ser His Val Asp Gly Ala Ala Lys Ser Leu Asp Lys Gln Lys Lys Lys
130          210          215          220

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132 Pro Lys Met Thr Asp Glu Glu Ile Met Glu Lys Leu Arg Thr Ile Val
133 225                230                235                240
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136                245                250                255
138 Gln Gly Ala Ser Gly Thr Val Phe Thr Ala Thr Asp Val Ala Leu Gly
139                260                265                270
141 Gln Glu Val Ala Ile Lys Gln Ile Asn Leu Gln Lys Gln Pro Lys Lys
142                275                280                285
144 Glu Leu Ile Ile Asn Glu Ile Leu Val Met Lys Glu Leu Lys Asn Pro
145                290                295                300
147 Asn Ile Val Asn Phe Leu Asp Ser Tyr Leu Val Gly Asp Glu Leu Phe
148 305                310                315                320
150 Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu Thr Asp Val Val Thr
151                325                330                335
153 Glu Thr Cys Met Asp Glu Ala Gln Ile Ala Ala Val Cys Arg Glu Cys
154                340                345                350
156 Leu Gln Ala Leu Glu Phe Leu His Ala Asn Gln Val Ile His Arg Asp
157                355                360                365
159 Ile Lys Ser Asp Asn Val Leu Leu Gly Met Glu Gly Ser Val Lys Leu
160                370                375                380
162 Thr Asp Phe Gly Phe Cys Ala Gln Ile Thr Pro Glu Gln Ser Lys Arg
163 385                390                395                400
165 Ser Thr Met Val Gly Thr Pro Tyr Trp Met Ala Pro Glu Val Val Thr
166                405                410                415
168 Arg Lys Ala Tyr Gly Pro Lys Val Asp Ile Trp Ser Leu Gly Ile Met
169                420                425                430
171 Ala Ile Glu Met Val Glu Gly Glu Pro Pro Tyr Leu Asn Glu Asn Pro
172                435                440                445
174 Leu Arg Ala Leu Tyr Leu Ile Ala Thr Asn Gly Thr Pro Glu Leu Gln
175                450                455                460
177 Asn Pro Glu Lys Leu Ser Pro Ile Phe Arg Asp Phe Leu Asn Arg Cys
178 465                470                475                480
180 Leu Glu Met Asp Val Glu Lys Arg Gly Ser Ala Lys Glu Leu Leu Gln
181                485                490                495
183 His Pro Phe Leu Lys Leu Ala Lys Pro Leu Ser Ser Leu Thr Pro Leu
184                500                505                510
186 Ile Met Ala Ala Lys Glu Ala Met Lys Ser Asn Arg
187                515                520
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192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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202 <210> SEQ ID NO: 6
203 <211> LENGTH: 53
204 <212> TYPE: DNA

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208 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
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239 <211> LENGTH: 3255
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241 <213> ORGANISM: Homo sapiens
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253 caactgctcc aggacagcaa gacaaaaata gaagtcatac gaatgcagat tcttcaggca 600
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255 cggatggaag aattaaggca tcatttttag atagagtttg cagtagcaga aggtgcaaag 720
256 aatgtaatga aattacttgg ctacggaaaa gtaacagaca gaaaagcact ttcagaagct 780
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267 caacggcatg gcatgtgtct ctatttggaa ccacagggta ctttatttgc agaggttacc 1440
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269 aagcaacaag gcaaaacatt tctcagagct cctcaaata atattaatat tgccacttgg 1560
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274 ataccaggac aggattcaga gactgttttt gatattcaga atgacagaaa tagtatactt 1860
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302 <211> LENGTH: 984

303 <212> TYPE: PRT

304 <213> ORGANISM: Homo sapiens

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311 20 25 30
313 Lys Leu Asp Phe Ser Asp Thr Met Val Gln Gln Lys Leu Asp Asp Ile
314 35 40 45
316 Lys Asp Arg Ile Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu
317 50 55 60
319 Gly Ala Glu Asn Leu Arg Lys Val Thr Thr Asp Lys Lys Ser Leu Ala
320 65 70 75 80
322 Tyr Val Asp Asn Ile Leu Lys Lys Ser Asn Lys Lys Leu Glu Glu Leu
323 85 90 95

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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date